



SEQUENCE LISTING

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TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.
- (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
11D10 AND METHODS OF USE THEREOF
- (iii) NUMBER OF SEQUENCES: 58
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: MORRISON & FOERSTER
 - (B) STREET: 755 PAGE MILL ROAD
 - (C) CITY: PALO ALTO
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Polizzi, Catherine M.
 - (B) REGISTRATION NUMBER: 40,130
 - (C) REFERENCE/DOCKET NUMBER: 30414-20003.21
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (415) 813-5600
 - (B) TELEFAX: (415) 494-0792
 - (C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 435 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..435

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA 48
Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
-20 -15 -10 -5

GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT 96
Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
1 5 10

GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC 144
Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
15 20 25

ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT 192
Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
30 35 40

AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA 240
Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
45 50 55 60

AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC 288
Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
65 70 75

AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT 336
Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
80 85 90

AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG 384
Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
95 100 105

GCT	GAT	GCT	GCA	CCA	ACT	GTA	TCC	ATC	TTC	CCA	CCA	TCC	AGT	AAG	CTT	432
Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Lys	Leu	.
110						115					120					

GGG 435
Gly
125

(2) INFORMATION FOR SEO ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
-20          -15          -10          -5

Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
          1          5          10

Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
          15          20          25

Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
          30          35          40

Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
          45          50          55          60

Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
          65          70          75

Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
          80          85          90

Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
          95          100          105

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
          110          115          120

Gly
125

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..459

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT
Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
-19          -15          -10          -5

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48

GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG	96
Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg	
1 5 10	
TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG	144
Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu	
15 20 25	
ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG	192
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu	
30 35 40 45	
GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT	240
Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn	
50 55 60	
CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC	288
Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser	
65 70 75	
ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC	336
Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
80 85 90	
TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT	384
Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly	
95 100 105	
CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC	432
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro	
110 115 120 125	
GTC TAT CCA CTG GTC CCT GGA AGC TTG GG	461
Val Tyr Pro Leu Val Pro Gly Ser Leu	
130	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly	
-19 -15 -10 -5	
Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg	
1 5 10	
Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu	
15 20 25	
Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu	

30	35	40	45
Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn			
50	55	60	
Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser			
65	70	75	
Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val			
80	85	90	
Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly			
95	100	105	
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro			
110	115	120	125
Val Tyr Pro Leu Val Pro Gly Ser Leu			
130			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
GATGGAAC TAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTGCCCAA	180
AGGTTCAAGT GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GANATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
GATGGAACCTT TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA	180
AGGTTCAAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT GTCCGTACAC GTTCGGAGGG	300
GGGACCAAGC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
GATGGAACCTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA	180
AGGTTCAAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
GGCACCAAGC TGGAAATCAA A	321

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120

GATGGA ACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA	180
AGGTT CAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
GGCACCAAGC TGGAAATCAA A	321

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGCCAAGTCA GGACATTGGT AGTAGCTTAA ACTGGCTTCA GCAGGAACCA	120
GATGGA ACTA TTAAACGCCT GATCTACGCC ACATCCAGTT TAGATTCTGG TGTCCCCAAA	180
AGGTT CAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG TAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTGGAC GTTCGGTGGA	300
GGCACCAAGC TGGAAATCAA A	321

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCCAGATGA CCCAGTCTCC ATCCTCCTTA TCTGCCTCTC TGGGAGAAAG AGTCAGTCTC	60
ACTTGTCGGG CAAGTCAGGA CATTGGTAGT AGCTTAAACT GGCTTCAGCA GGAACCAGAC	120
GGAAC TATTA AACGCCTGAT CTACGCCACA TCCAGTTTAG ATTCTGGTGT CCCC AAAAGG	180
TTCAGTGGCA GTAGGTCTGG GTCAGATTAT TCTCTACCA TCAGCAGCCT TGAGTCTGAA	240
GATTTTGTAG ACTATTACTG TCTACAATAT GCTAGTTCTC CGTGGACGTT CGGTGGAGGC	300

ACCAAGCTGG AAATCAAA

318

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT	60
CAGGACATTG GTAGTAGCTT AAAGTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC	120
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCAG TGGCAGTAGG	180
TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAGT CTGAAGATTT TGTAGACTAT	240
TACTGTCTAC AATATGCTAG TTCTCCGTAC ACGTTCGGAG GGGGGACCAA GCTGNAAATA	300
AAA	303

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTACTTAA GCTGGCTTCA GCAGAAACCA	120
GATGGAAC TAACGCCT GATCTACAGC ACATCCACTT TAAATTCTGG TGTCCCAAAA	180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG CAGACTATTA CTGTCTACAA TATGCTAGTT CTCCGTACAC GTTCGGAGGG	300
GGGACCAAAC TGGAAATAAA A	321

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TCTCCATCCT CCTTATCTGC CTCTCTGGGA GAAAGAGTCA GTCTCACTTG TCGGGCAAGT	60
CAGGACATTG GTAATAGCTT AAAGTGGCTT CAGCAGGAAC CAGATGGAAC TATTAAACGC	120
CTGATCTACG CCACATCCAG TTTAGATTCT GGTGTCCCCA AAAGGTTTCAG TGGCAGTAGG	180
TCTGGGTCAG ATTATTCTCT CACCATCAGC AGCCTTGAAT CTGAAGATTT TGTAGTCTAT	240
TACTGTCTAC AATATGCTAG TTATACGTAC ACGTTCGGAG GGGGGACCAA GTTGGAACATA	300
AAA	303

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GACATCCAGA TGACCCAGTC TCCATCCTCC TTATCTGCCT CTCTGGGAGA AAGAGTCAGT	60
CTCACTTGTC GGGCAAGTCA GGAAATTAGT GGTACTTAA GCTGGCTTCA GCAGAAACCA	120
GATGGAACATA TTAAACGCCT GATCTACGCC GCATCCACTT TAGATTCTGG TGTCCCAAAA	180
AGGTTTCAGTG GCAGTAGGTC TGGGTCAGAT TATTCTCTCA CCATCAGCAG CCTTGAGTCT	240
GAAGATTTTG CAGACTATTA CTGTCTACAA TATCTTAGTT ATCCGCTCAC GTTCGGTGCT	300
GGGACCAAGC TGGAGCTGAA A	321

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAGGCTTATN TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG	60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA	120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC	180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGA	294

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA	46
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGGCTTATG TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG	60
TCCTGCAAGG CTTCTGGCTA CAGATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA	120
CGTAGACAGG GCCTGGAATG GATTGGAGCA ATTTATCCAG GAAATGGTGA TACTTCCTAT	180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ATTGTAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGAGAGG	300
GGTAACTACG TAGGACATAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC CGTCTCCTCA	360

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTAAGGC CTGGGTCCTC AGTGAAGATG	60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA	120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC	180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGGGGAT	300
TACTCCGGTA GTATAGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC CTCA	354

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG	60
TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA	120
CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC	180
AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC	240
ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG	297

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTGGGGCACA GGGACCACGG TCACCGTCTC C

31

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGGCTTATC TACAGCAGTC TGGGGCTGAG CTGGTGAGGC CTGGGGCCTC AGTGAAGATG 60

TCCTGCAAGG CTTCTGGCTA CACATTTACC AGTTACAATA TGCACTGGGT AAAGCAGACA 120

CCTAGACAGG GCCTGGAATG GATTGGAGCT ATTTATCCAG GAAATGGTGA TACTTCCTAC 180

AATCAGAAGT TCAAGGGCAA GGCCACACTG ACTGTAGACA AATCCTCCAG CACAGCCTAC 240

ATGCAGCTCA GCAGCCTGAC ATCTGAAGAC TCTGCGGTCT ATTTCTGTGC AAGAGTG 297

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGGGGCACA GGGACCACGG TCACCGTCTC

30

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGGTCCAGCT GCAGCAGTCT GGACCTGAGC TGGTAAAGCC TGGGGCTTCA GTGAAGATAT	60
CCTGCAAGGC TTCTGGATAC ACATTCCTG ACTACTACAT GCACTGGGTG AAGCAGAAGC	120
CTGGGCAGGG CCTTGAGTGG ATTGGAGAGA TTTATCCTGG AAGTGGTAAT ACTTACTACA	180
ATGAGAAGTT CAAGGGYAAG GCCTCACTGA CTGCAGACAA ATCCTCCAGC ACAGCCTACA	240
TGCAGCTCAG CAGCCTGACA TCTGAGGACT CTGCAGTCTA TTTCTGTGCA AGACGTTACT	300

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA	46
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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG	60
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG	120
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC	180
ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGAG	295

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG 60
 TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG 120
 CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC 180
 ACTCAGAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC 240
 ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA 294

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA 46

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGGTTTCAGC TCCAGCAGTC TGGGGCTGAG CTGGCAAGAC CTGGGGCTTC AGTGAAGTTG	60
TCCTGCAAGG CTTCTGGCTA CACCTTTACT AGCTACTGGA TGCAGTGGGT AAAACAGAGG	120
CCTGGACAGG GTCTGGAATG GATTGGGGCT ATTTATCCTG GAGATGGTGA TACTAGGTAC	180
ACTCAGAAAGT TCAAGGGCAA GGCCACATTG ACTGCAGATA AATCCTCCAG CACAGCCTAC	240
ATGCAACTCA GCAGCTTGGC ATCTGAGGAC TCTGCGGTCT ATTACTGTGC AAGA	294

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA	46
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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGTCCAAC TGCAGCAGCC TGGTGCTGAG CTTGTGAAGC CTGGGGCCTC AGTGAAGCTG	60
TCCTGCAAGG CTTCTGGCTA CACTTTCACC AGCTACTGGA TAAACTGGGT GAAGCAGAGG	120
CCTGGACAAG GCCTTGAGTG GATTGGAAAT ATTTATCCTG GTAGTAGTAG TACTAACTAC	180
AATGAGAAGT TCAAGAGCAA GGCCACACTG ACTGTAGACA CATCCTCCAG CACAGCCTAC	240
ATGCAGCTCA GCAGCCTGAC ATCTGACGAC TCTGCGGTCT ATTATTGTGC AAGACG	296

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGCTATGGAC TACTGGGGTC AAGGAACCTC AGTCACCGTC TCCTCA

46

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "May also be the amino acid
arginine(R) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "May also be the amino acid
glutamine(E) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 16
 (D) OTHER INFORMATION: /note= "May also be the amino acid
serine(S) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "May also be the amino acid
proline(P) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
1 5 10 15

Arg Pro Ala Pro
 20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "May also be the amino acid arginine(R) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "May also be the amino acid glutamine(E) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "May also be the amino acid serine(S) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 22
- (D) OTHER INFORMATION: /note= "May also be the amino acid proline(P) "

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "May also be the amino acid proline(P) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala
1				5				10						15	
Pro Asp Thr Arg Pro Ala Pro															
20															

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc_difference
- (B) LOCATION: replace(30, "")
- (D) OTHER INFORMATION: /note= "N represents the nucleotide Inosine"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG

35

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGGAATTCAT GRAATGSASC TGGGTYWTYC TCTT

34

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTTTTCCCAG TCACGACGT

19

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGNWTCTT

42

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CAGATGGAAG GGCCCAAC

18

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATTGATGCA TATCATTACC

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTATCGATG TCGAATAGCC

20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTGCTGCAGA TTGAGTACTG TTCT

24

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp Ile Gly Ser Ser
 20 25 30

Leu Asn Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile Lys Arg Leu Ile
 35 40 45

Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro Lys Arg Phe Ser Gly
 50 55 60

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80

Gly Asp Phe Val Asp Tyr Tyr Cys Leu Gln Tyr Ala Ser Ser Pro Tyr
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30
Trp Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Asn Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr
65 70 75 80
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
85 90 95
Ala Arg Gly Xaa Xaa Xaa Gly Ala Met Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Ser Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /note= "position 54-57 of 11D10
comparison sequence #8 (Fig. 26B) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Asp Ser Tyr
1

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "positions 118-126 of 11d10 comparison sequence #2 and positions 100-108 of 11d10 comparison sequence #6 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /note= "positions 99-105 of 11D10 comparison sequence #3 and #8 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
- (B) LOCATION: 1..4
- (D) OTHER INFORMATION: /note= "positions 100-103 of 11D10 comparison sequence #12 (Fig. 26B)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Val Tyr Tyr Tyr
1

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #14 (Fig. 26B) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Phe Tyr Phe Tyr
1

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Region
(B) LOCATION: 1..4
(D) OTHER INFORMATION: /note= "positions 100-103 of 11D10
comparison sequence #15 (Fig. 26B) "

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Leu Phe Thr
1

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Ser Thr Ala Pro Pro Ala His Arg Val Thr Ser Ala Pro Glu Ser
1 5 10 15
Arg Pro Pro Pro
20

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Pro Pro Arg Ser Glu Pro Ala Ser Thr Val Arg His Ala Pro Pro
1 5 10 15
Ala Thr Ser Gly
20

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ala Pro Asp Thr Arg Pro Pro Pro
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met	Gly	Thr	Pro	Ala	Gln	Ile	Leu	Gly	Phe	Leu	Leu	Leu	Leu	Phe	Pro
1				5					10					15	
Gly	Thr	Arg	Cys	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser
			20					25					30		
Ala	Ser	Leu	Gly	Gln	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	Asp
		35					40				45				
Ile	Gly	Ile	Asn	Leu	His	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	Ile
	50					55					60				
Lys	Arg	Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Gly	Ser	Gly	Val	Pro	Lys
65					70					75					80
Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	Ser
				85					90					95	
Ser	Leu	Glu	Ser	Gly	Asp	Phe	Val	Ala	Tyr	Tyr	Cys	Leu	Gln	Tyr	Ala
			100					105					110		
Ser	Ser	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg
		115					120					125			
Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Lys	Leu
	130					135					140				
Gly															
145															